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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Oct 25 18:17:00 EDT 2007

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Reviewer Comments:

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<212> PRT

<213> Artificial sequence

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<223> Synthetic peptide

<220>

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<222> (13)..(14)

<223> D-Val

<220>

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<222> (17)..(17)

<223> D-Val

<400> 17

Phe	Ser	Glu	Pro	Glu	Ile	Thr	Leu	Ile	Ile	Phe	Gly	Val	Met	Ala	Gly
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Val	Ile	Gly	Thr	Ile	Leu	Leu	Ile	Ser	Tyr	Gly	Ile	Arg	Arg	Leu	Ile
			20					25						30	

One of the above <222> lines indicates Val at locations 13 and 14; Val

is only at location 13. Met is at location 14.

<210> 25
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<222> (17)..(17)
<223> D-Ala

<400> 25

Lys Lys Ile Thr Ala Gly Ala Ala Gly Val Ala Ala Gly Val Ala Ala
1 5 10 15

Ala

One of the above <223> lines indicates "D-Glu" at location 6: "Gly" is
at location 6.

Application No: 10583996 Version No: 2.0

Input Set:**Output Set:**

Started: 2007-10-09 10:33:48.696
Finished: 2007-10-09 10:33:50.314
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 618 ms
Total Warnings: 29
Total Errors: 0
No. of SeqIDs Defined: 29
Actual SeqID Count: 29

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Input Set:

Output Set:

Started: 2007-10-09 10:33:48.696
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Total Errors: 0
No. of SeqIDs Defined: 29
Actual SeqID Count: 29

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Yeda Research and Development Co. Ltd. at the Weizmann
Institute of Science

<120> Diastereomeric Peptides Useful As Inhibitors of Membrane Protein
Assembly

<130> YEDA/038 PCT

<140> 10583996

<141> 2007-10-09

<150> US 60/530,899

<151> 2003-12-22

<160> 29

<170> PatentIn version 3.3

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Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
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Trp Asn Trp Phe
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Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
20 25 30

Trp Asn Trp Phe
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Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu
20 25 30

Trp Asn Trp Phe
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Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly Ala Ala Gly
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Leu

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<222> (14)..(14)

<223> D-Ala

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Ser Thr Met Gly Ala Arg Ser Met Thr Leu Thr Val Gln Ala Arg Gln
20 25 30

Leu

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Leu

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Leu

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Lys Lys Ile Thr Leu Ile Ile Phe Gly Val Met Ala Gly Val Ile Gly
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Thr

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Thr Lys Lys

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Thr

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Thr

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Thr Lys Lys

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Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Leu Ile
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Met Ala Gly Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Arg
20 25 30

Arg Leu Ile
35

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Val Ile Gly Thr Ile Leu Leu Ile Ser Tyr Gly Ile Arg Arg Leu Ile
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Gly Ser Leu Lys Lys
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<222> (18)..(18)

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<400> 23

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Gly Ser Leu Lys Lys
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Ala Val Gly Ile Gly Ala Leu Phe
1 5

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Lys Lys Ile Thr Ala Gly Ala Ala Gly Val Ala Ala Gly Val Ala Ala
1 5 10 15

Ala

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<400> 26

Trp Met Glu Trp Asp Arg Glu Ile Asn Asn Tyr Thr Ser Leu Ile His
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Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu
20 25 30

Leu Leu

<210> 27
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Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly
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Ala Gln Ile Thr Ala Gly Ile Ala Leu Ala Glu Ala Arg Glu Ala Lys
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Arg

<210> 29

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1 5 10 15

Gly Ser Leu Lys Lys
20